

```

1 MAPGWPRSLPQILVLGFLVLMRAAAGEQAPGTSPCSSGSSWSADLDKCM 50
|| | | | : || | | | : | | | | | | | | | | | | | | | |
1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAPCSRGSWSADLDKCM 50

. . . . .
51 DCASCPARPHSDFCLGCAAAPPAHFRLLWPILGGALSLVLVLALVSSFLV 100
|||| | | | | | | | | | | | | | | | | | | | | | | | | | |
51 DCASCRARPHSDFCLGCAAAPPAFRLLPILGGALSLTFVLGLLSGFLV 100

. . .
101 WRRCCRREKFTTPIEETGGEGCPCGVALIQ 129
|||| | | | | | | | | | | | | | | | | | | | | | | | | | |
101 WRRCCRREKFTTPIEETGGEGCPCPAVALIQ 129

```

Fig. 1

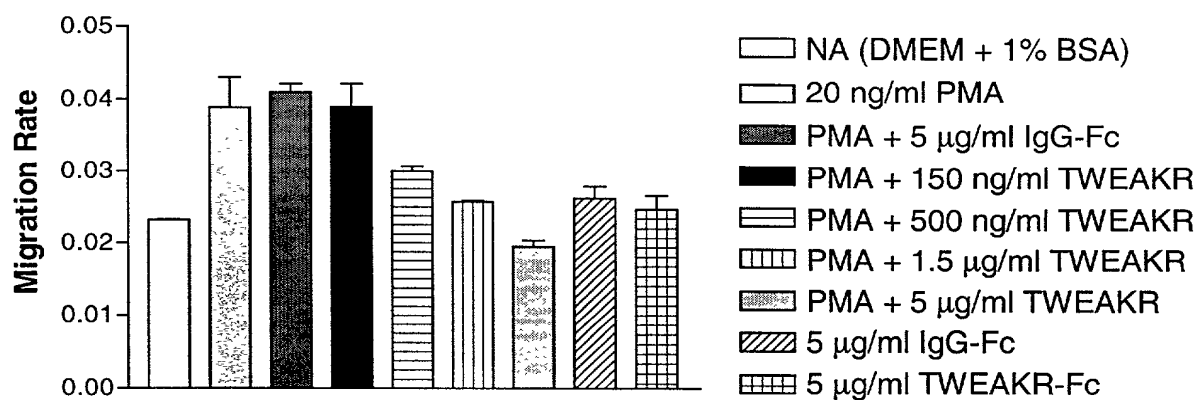


Fig. 2

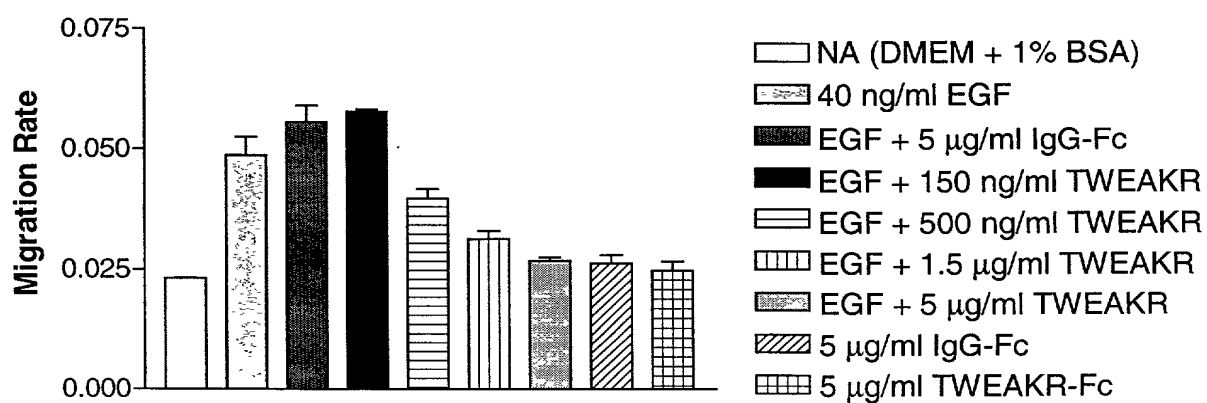


Fig. 3

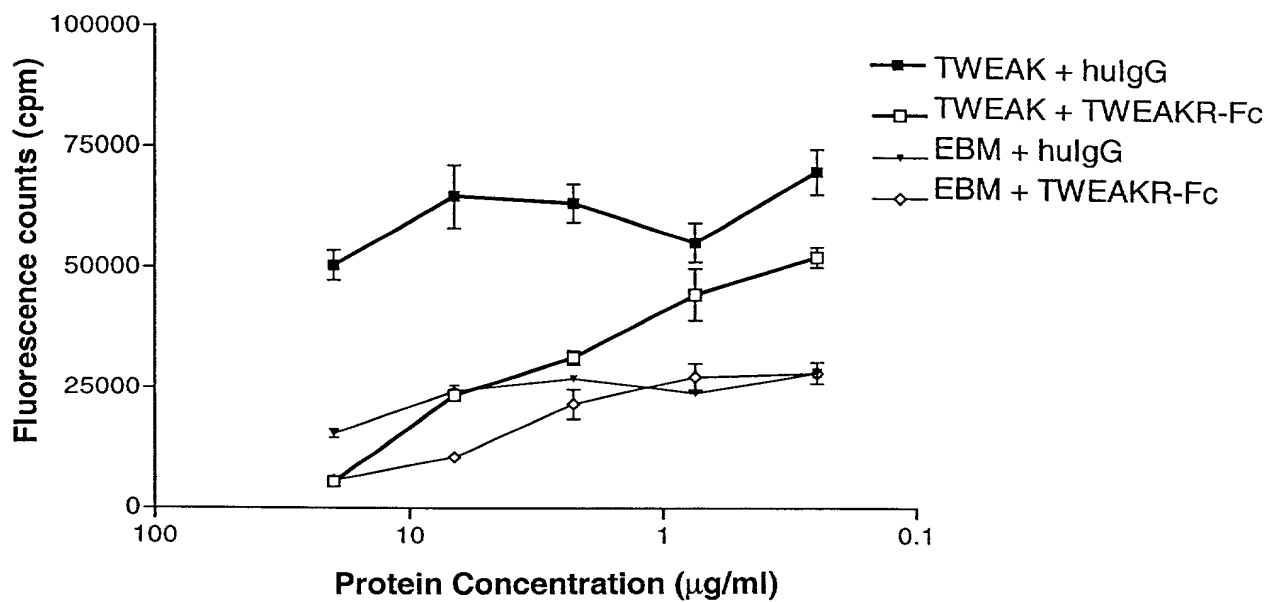


Fig. 4

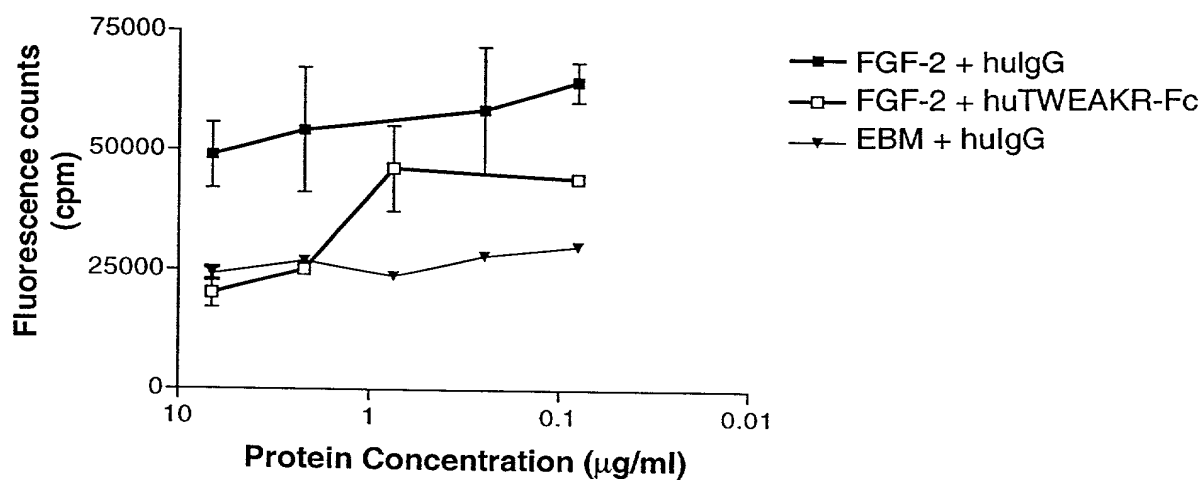


Fig. 5